

WHAT IS CLAIMED IS:

1. A method of determining the amino acid sequence of a polypeptide characterized in that it comprises:
 - (a) derivatizing the N-terminus of the polypeptide or the N-termini of one or more peptides of the polypeptide with one or more acidic moieties having pKas of less than 2, preferably less than 0, more preferably less than -2 when coupled with the polypeptide or peptides, to provide one or more derivatized analytes;
 - (b) analyzing one or more derivatized analytes using a mass spectrometric technique to provide a fragmentation pattern, preferably the fragmentation pattern is substantially free of a-ions and b-ions; and
 - (c) interpreting the fragmentation pattern.
2. A method according to Claim 1 characterized in that the mass spectrometric technique is MALDI PSD mass spectrometry, preferably positive ion mode PSD MALDI; or electrospray ionization tandem mass spectrometry, preferably tandem electrospray ionization mass spectrometry.
3. A method according to Claim 1 or 2 characterized in that interpretation of the fragmentation pattern comprises using a commercially available software program or database.
4. A method according to any of Claims 1-3 characterized in that the polypeptide is a synthetic polypeptide.
5. A method according to any of Claims 1-4 characterized in that the peptides of the polypeptide are produced by digestion, preferably the digestion is chemical digestion, more preferably the chemical digestion is cyanogen bromide digestion.
6. A method according to Claim 5 characterized in that the digestion is enzymatic digestion, preferably the enzymatic digestion is selected from endoproteinase Lys C digestion, endoproteinase Arg C digestion, tryptic digestion, and chymotryptic digestion.

7. A method according to any of Claims 1-6 characterized in that the acidic moiety is one or more sulfonic acids or a disulfonic acid derivative, preferably the acidic moiety is a 2-sulfoacetyl moiety, a 3-sulfopropionoyl moiety, or a 2-sulfobenzoyl moiety.
8. A kit for use in determining the amino acid sequence of a polypeptide characterized in that it comprises:
 - (a) one or more acidic moiety reagents providing one or more acidic moieties having pK_as of less than 2 when coupled with the polypeptide or one or more peptides of the polypeptide; and
 - (b) means for derivatizing the N-terminus of the polypeptide or the N-termini of one or more peptides of the polypeptide with one or more acidic moiety reagents.
9. A kit according to Claim 8 characterized in that the means for derivatizing comprises one or more containment devices, preferably the acidic moiety reagent resides within the containment devices; preferably the means for derivatizing further comprises a buffer system.
10. A kit according to Claim 8 or 9 characterized in that it further comprises one or more digestion aids.